

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 06:26:26 ; Search time 188.13 Seconds
(without alignments)
59.035 Million cell updates/sec

Title: US-09-856-050-19

Perfect score: 220
Sequence: 1 MNLILITFVAANAARFDDDKLVHGKLNHHHHDDDK 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_Main: *
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2: /cgn2_6/ptodata/2/paa/US06_COMB.pep: *
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24: /cgn2_6/ptodata/2/paa/US060_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	40	22	US-09-856-050-19
2	122	55.5	247	23	US-09-923-779-154
3	122	55.5	247	24	US-60-230-435-1545
4	112	50.9	247	1	PCR-US00-28558-4
5	112	50.9	247	18	US-09-418-527C-4
6	112	50.9	280	24	US-60-212-659-307
7	112	50.9	280	24	US-60-230-435-1884
8	110	50.0	251	21	US-09-760-475-2344
9	104	47.3	180	24	US-60-213-800-342

10	102	46.4	247	24	US-60-212-659-308	Sequence 308, App
11	102	46.4	247	24	US-60-230-435-1885	Sequence 1885, Ap
12	98	44.5	247	21	US-09-760-475-2359	Sequence 2359, Ap
13	91	41.4	247	21	US-09-762-277-1	Sequence 1, Appl
14	90	40.9	53	20	US-09-605-784A-1262	Sequence 1262, Ap
15	86	39.1	45	22	US-09-856-050-17	Sequence 17, Appl
16	84	38.2	281	8	US-08-467-155-7	Sequence 7, Appl
17	81	36.8	246	13	US-08-978-404A-44	Sequence 44, Appl
18	79	35.9	20	20	US-09-674-677-34	Sequence 34, Appl
19	77	35.0	183	10	US-08-691-274-9	Sequence 9, Appl
20	76	34.5	76	22	US-09-869-446-2	Sequence 2, Appl
21	76	34.5	124	22	US-09-869-446-9	Sequence 9, Appl
22	75.5	34.3	401	19	US-09-538-092-572	Sequence 572, App
23	75	34.1	51	1	PCR-US00-05989-566	Sequence 566, App
24	75	34.1	51	23	US-09-925-297-566	Sequence 566, App
25	74	33.6	284	1	PCR-US00-22283-54	Sequence 54, Appl
26	74	33.6	284	17	US-09-386-642-54	Sequence 54, Appl
27	74	33.6	288	1	PCR-US00-09973-13	Sequence 13, Appl
28	74	33.6	288	1	PCR-US00-22271-13	Sequence 13, Appl
29	74	33.6	288	1	PCR-US00-22283-13	Sequence 13, Appl
30	74	33.6	288	1	PCR-US00-22283-13	Sequence 13, Appl
31	74	33.6	288	17	US-09-303-162-13	Sequence 13, Appl
32	74	33.6	288	17	US-09-386-642-13	Sequence 13, Appl
33	74	33.6	289	1	PCR-US00-09973-14	Sequence 14, Appl
34	74	33.6	289	1	PCR-US00-22271-14	Sequence 14, Appl
35	74	33.6	289	1	PCR-US00-22283-14	Sequence 14, Appl
36	74	33.6	289	17	US-09-303-162-14	Sequence 14, Appl
37	74	33.6	289	17	US-09-386-642-14	Sequence 14, Appl
38	74	33.6	292	1	PCR-US01-18568-9	Sequence 9, Appl
39	74	33.6	292	1	PCR-US01-18568A-9	Sequence 9, Appl
40	74	33.6	315	1	PCR-US00-23843-9	Sequence 9, Appl
41	74	33.6	315	17	US-09-386-653-9	Sequence 9, Appl
42	74	33.6	315	17	US-09-386-653A-9	Sequence 9, Appl
43	74	33.6	316	17	US-09-387-375-9	Sequence 9, Appl
44	74	33.6	327	17	US-09-386-659-8	Sequence 8, Appl
45	74	33.6	328	1	PCR-US00-09973-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-856-050-19
; Sequence 19, Application US/09856050
; GENERAL INFORMATION:
; APPLICANT: UEMURA, Hidetoshi
; APPLICANT: OKUI, Akira
; APPLICANT: KOMINAMI, Katsuya
; APPLICANT: YAMAGUCHI, Nozomi
; APPLICANT: MITSUI, Shinichi
; TITLE OF INVENTION: PROTEIN EXPRESSION VECTOR AND USE THEREOF
; FILE REFERENCE: UEMURA=8
; CURRENT APPLICATION NUMBER: US/09/856, 050
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: JP 10/331515
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCR/JP99/06474
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Synthetic
; US-09-856-050-19

Query Match 100.0% Score 220; DB 22; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT      4
PCR-US00-28558-4
: Sequence 4, Application PC/TUS0028558
: GENERAL INFORMATION:
: APPLICANT: O'Brien, Timothy J.
: APPLICANT: Underwood, Lowell
: APPLICANT: Shigemasa, Kazushi
: TITLE OF INVENTION: Tumor Antigen-Derived Gene 16 (TADG-16): A Novel
: TITLE OF INVENTION: Extracellular Serine Protease and Uses Thereof

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RESULT      6
US-60-212-659-307
: Sequence 307, Application US/60212659
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: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CLO00674
: CURRENT APPLICATION NUMBER: US/60/212,659
: CURRENT FILING DATE: 2000-06-19
: NUMBER OF SEQ ID NOS: 879
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 307
:
: LENGTH: 280
:
: TYPE: PRT
: ORGANISM: HUMAN
: US-60-212-659-307

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Query Match 50.9%; Score 112; DB 24; Length 280;
Best Local Similarity 85.2%; Pred. No. 6.6e-06;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNLLILTFVAAAVAPFDDDDKLVHG 27
|||
DB 1 MNPLILTFVAAALAPFDDDDKIVGG 27

RESULT 7
US-60-230-435-1884
; Sequence 1884, Application US/60230435
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: C1000768
; CURRENT APPLICATION NUMBER: US/60/230,435
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 2991
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1884
; LENGTH: 280
; TYPE: PRT
; ORGANISM: HUMAN
US-60-230-435-1884

Query Match 50.9%; Score 112; DB 24; Length 280;
Best Local Similarity 85.2%; Pred. No. 6.6e-06;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNLLILTFVAAAVAPFDDDDKLVHG 27
|||
DB 1 MNPLILTFVAAALAPFDDDDKIVGG 27

RESULT 8
US-09-760-475-2344
; Sequence 2344, Application US/09760475
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT249
; CURRENT APPLICATION NUMBER: US/09/760,475
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2344
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (18)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-475-2344

Query Match 50.0%; Score 110; DB 21; Length 251;

Best Local Similarity 85.2%; Pred. No. 1.1e-05;
Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNLLILTFVAAAVAPFDDDDKLVHG 27
|||
DB 5 MNPLILTFVAAAXAPFDDDDKIVGG 31

RESULT 9
US-60-213-800-342
; Sequence 342, Application US/60213800
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: C1000707
; CURRENT APPLICATION NUMBER: US/60/213,800
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 657
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 180
; TYPE: PRT
; ORGANISM: HUMAN
US-60-213-800-342

Query Match 47.3%; Score 104; DB 24; Length 180;
Best Local Similarity 87.5%; Pred. No. 4.3e-05;
Matches 21; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LILTFVAAAVAPFDDDDKIVHG 27
|||||
DB 1 LILTFVAAALAPFDDDDKIVGG 24

RESULT 10
US-60-212-659-308
; Sequence 308, Application US/60212659
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: C1000674
; CURRENT APPLICATION NUMBER: US/60/212,659
; CURRENT FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 879
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 247
; TYPE: PRT
; ORGANISM: HUMAN
US-60-212-659-308

Query Match 46.4%; Score 102; DB 24; Length 247;
Best Local Similarity 77.8%; Pred. No. 0.00011;
Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNLLILTFVAAAVAPFDDDDKLVHG 27
|||
DB 1 MNPLILTFVAAAVAPFDDDDKIVGG 27

RESULT 11
US-60-230-435-1885
; Sequence 1885, Application US/60230435
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

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RESULT 15
US-09-856-050-17
: Sequence 17, Application US/09856050
: GENERAL INFORMATION:
: APPLICANT: DEMURA, Hirotoshi
: APPLICANT: OKUI, Akira
: APPLICANT: KOMINAMI, Katsuya
: APPLICANT: YAMAGUCHI, Nozomi
: APPLICANT: MITSUI, Shinichi
: TITLE OF INVENTION: PROTEIN EXPRESSION VECTOR AND USE THEREOF
: FILE REFERENCE: DEMURA-8
: CURRENT APPLICATION NUMBER: US/09/856,050
: CURRENT FILING DATE: 2001-05-17
: PRIOR APPLICATION NUMBER: JP 10/331515
: PRIOR FILING DATE: 1998-11-20
: PRIOR APPLICATION NUMBER: PCT/JP99/06474
: PRIOR FILING DATE: 1999-11-19
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 17
: LENGTH: 45

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-856-050-17

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Query Match      39.1%; Score 86; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 KLNHHHHHDDDDK 40
DB 33 KLNHHHHHDDDDK 45

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Search completed: March 15, 2002, 06:48:48
Job time: 1342 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 06:26:26 ; Search time 17.14 Seconds

(without alignments)
148.848 Million cell updates/sec

Title: US-09-856-050-19
Perfect score: 220

Sequence: 1 MNLLILTFVAAAVAAFPDDDDKLVHGKLNHHHHDDDK 40

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 302707 seqs, 63781257 residues

Total number of hits satisfying chosen parameters: 302707

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep1:*
7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	50.9	247	6	US-09-907-187A-4
2	91	41.4	247	6	US-09-762-277A-1
3	84	38.2	246	6	US-09-831-180A-53
4	84	38.2	246	6	US-09-842-758-55
5	84	38.2	281	7	US-10-021-368-7
6	75.5	34.3	401	6	US-09-550-398C-104
7	75.5	34.3	401	6	US-09-911-882-20
8	75.5	34.3	401	6	US-09-911-888-20
9	75.5	34.3	401	6	US-09-911-927-20
10	74	33.6	198	6	US-09-708-427-49415
11	74	33.6	315	7	US-10-040-655-9
12	74	33.6	315	7	US-10-041-006-9
13	74	33.6	327	7	US-10-040-803-8
14	72	32.3	149	6	US-09-620-111B-5168
15	71	32.3	132	6	US-09-708-427-58802
16	69	31.4	85	6	US-09-620-111B-1590
17	69	31.4	90	6	US-09-620-111B-1589
18	69	31.4	94	6	US-09-620-111B-8431
19	69	31.4	106	6	US-09-620-111B-133
20	69	31.4	111	6	US-09-620-111B-132
21	69	31.4	114	6	US-09-620-394B-8
22	69	31.4	114	6	US-09-620-111B-4893
23	69	31.4	119	6	US-09-620-111B-4892
24	69	31.4	121	6	US-09-620-111B-7542
25	69	31.4	126	6	US-09-620-111B-7541

26	69	31.4	134	6	US-09-620-111B-1588	Sequence 1588, Ap
27	69	31.4	151	6	US-09-620-111B-4891	Sequence 4891, Ap
28	69	31.4	155	6	US-09-620-111B-131	Sequence 131, App
29	69	31.4	156	6	US-09-620-111B-7540	Sequence 7540, Ap
30	68	30.9	195	6	US-09-284-101-4	Sequence 4, Appl
31	68	30.9	199	6	US-09-708-427-55401	Sequence 55401, A
32	68	30.9	231	6	US-09-708-427-55400	Sequence 55400, A
33	68	30.9	281	6	US-09-708-427-55399	Sequence 55399, A
34	67.5	30.7	127	6	US-09-481-620A-40	Sequence 40, Appl
35	67.5	30.7	127	6	US-09-481-620A-72	Sequence 72, Appl
36	67.5	30.7	131	6	US-09-708-427-82155	Sequence 82155, A
37	67.5	30.7	207	6	US-09-708-427-82154	Sequence 82154, A
38	67.5	30.7	218	6	US-09-708-427-82153	Sequence 82153, A
39	67	30.5	246	6	US-09-762-277A-2	Sequence 2, Appl
40	66.5	30.2	20	1	PCR-US01-44516-5	Sequence 5, Appl
41	66.5	30.2	24	6	US-09-613-972-22	Sequence 22, Appl
42	66.5	30.2	24	7	US-10-080-455-5	Sequence 5, Appl
43	66	30.0	23	6	US-09-939-126-7	Sequence 7, Appl
44	66	30.0	88	6	US-09-614-150-29439	Sequence 29439, A
45	66	30.0	109	6	US-09-380-913-33	Sequence 33, Appl

ALIGNMENTS

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RESULT 1
US-09-907-187A-4
; Sequence 4, Application US/09907187A
; GENERAL INFORMATION:
; APPLICANT: Underwood, Lowell
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Shigemasa, Kazushi
; TITLE OF INVENTION: Tumor Antigen-Derived Gene 16 (TAG-16): A Novel
; FILE OF INVENTION: Extracellular Serine Protease and Uses Thereof
; FILE REFERENCE: D6250D
; CURRENT APPLICATION NUMBER: US/09/907,187A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 09/418,527
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 4
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; OTHER INFORMATION: Sequence of Trypsinogen
US-09-907-187A-4

Query Match          50.9%; Score 112; DB 6; Length 247;
Best Local Similarity 85.2%; Pred. No. 4.5e-08;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNLLILTFVAAAVAAFPDDDDKLVHG 27
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DB 1 MNPLILTFVAAALAAFPDDDDKLVGG 27

RESULT 2
US-09-762-277A-1
; Sequence 1, Application US/09762277A
; GENERAL INFORMATION:
; APPLICANT: Fuji Yakuhin Kogyo Kabushiki Kaisha
; TITLE OF INVENTION: Monoclonal Antibody against Canine Trypsin
; FILE REFERENCE: FJ-94PCT
; CURRENT APPLICATION NUMBER: US/09/762,277A
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: JP 10-236609
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: JP 11-63990
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5

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RESULT 4
US-09-842-758--55
: Sequence 55, Application US/09842758
: GENERAL INFORMATION:
: APPLICANT: Vernet, Corine A. M.
: APPLICANT: Fernandes, Elma R
: APPLICANT: Gerlach, Valerie
: APPLICANT: Shinkets, Richard A
: APPLICANT: Malyankar, Uriel M
: APPLICANT: Boldog, Ferenc L
: APPLICANT: Zernhusen, Bryan D
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Majumder, Kundu
: APPLICANT: Tchernev, Velizar T
: APPLICANT: Padigar, Muralidhara
: APPLICANT: Patturajan, Meera
: APPLICANT: Burgess, Catherine E
: APPLICANT: Gangoli, Esna A
: APPLICANT: Smithson, Glenda
: APPLICANT: Rastelli, Luca
: APPLICANT: Macdougall, John R
: APPLICANT: Taupier, Raymond J
: APPLICANT: Grosse, William M
: APPLICANT: Edward, Szekeres S

RESULT 5
 US-10-021-368-7
 Sequence 7, Application US/10021368
 GENERAL INFORMATION:
 APPLICANT: Band, Yimla
 TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
 MOLECULES AND METHODS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/021.368

FILING DATE: 12-Dec-2001
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/201,038
 FILING DATE: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 00398/100002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-021-368-7

Query Match	38.2%	Score 84	DB 7	Length 281
Best Local Similarity	66.7%	Pred. No. 0.00044		
Matches	18	Conservative	2	Mismatches 7; Indels 0; Gaps 0
Qy	1	MNLLILTFVAAVAAPFPDDDKITVHG	27	
		:		
Db	1	MSALLILALVGAVAAPFPVDDDKITVGG	27	

```

RESULT      6
US-09-550-398C-104
: Sequence 104, Application US/09550398C
:
GENERAL INFORMATION:
: APPLICANT: Kurnasov, Oleg
: APPLICANT: Overbeek, Ross
: APPLICANT: Shatalin, Konstantin
: APPLICANT: Osterman, Andrei
: TITLE OF INVENTION: Novel Nicotinamide Mononucleotide Adenyltransferases
: FILE REFERENCE: 2002.0030000
: CURRENT APPLICATION NUMBER: US/09/550,398C
: CURRENT FILING DATE: 2000-04-14
: NUMBER OF SEQ ID NOS: 154
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 104
: LENGTH: 401
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-09-550-398C-104

```

Query Match	34.3%	Score 75.5	DB 6	length 401
Best Local Similarity	39.5%	Pred. No. 0.011		
Matches	15	Conservative	7	Mismatches 13; Indels 3; Gaps 1
Qy	6	ILTFVAALVAFEDDDDKLVHGCKLNNNNNNH---	DDDDK	40
Db	38	VLADANSSIDAEFNITKRKKKHHNNHHNNHRSKEGDK		75

```

US-09-911-882-20
:
: RESULT 7
:
: Sequence 20, Application US/09911882
:
: GENERAL INFORMATION:
:
: APPLICANT: Koltin, Yigal
:
: APPLICANT: Gavriels, Victoria
:
: TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
:
: FILE REFERENCE: 06286-062004
:
: CURRENT APPLICATION NUMBER: US/09/911,882
:
: CURRENT FILING DATE: 2001-07-23

```

```

? PRIOR APPLICATION NUMBER: US 08/965,762
?
? FILING DATE: 1997-11-07
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO: 20
? LENGTH: 401
? TYPE: prt
? ORGANISM: Saccharomyces cerevisiae
?
? US-09-911-862-20

```

	Query Match	34.3%	Score 75.5;	DB 6;	length 401;
	Best Local Similarity	Pred. No. 0.011;			
	Matches 15; Conservative	7;	Mismatches 13;	Indels 3;	Gaps 1
Oy	6 ILTFVAALVAFPPDDDKLVNGHGLNNNNN---DDDDK	40			
	: : : : : : : : : : : : : : : :				
Dd	38 VLADANSSIDAPFNJRKRRKKNNNNNNNNNNNSKEGCDK	75			

```

RESULT      8
US-09-911-888-20
: Sequence 20, Application US/09911888
: GENERAL INFORMATION:
:   APPLICANT: KOLTEIN, YIGAL
:   APPLICANT: GAVRIAS, VICTORIA
:   TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
:   FILE REFERENCE: 06286-062002
:   CURRENT APPLICATION NUMBER: US/09/911,888
:   CURRENT FILING DATE: 2001-07-23
:   PRIOR APPLICATION NUMBER: US 08/965,762
:   PRIOR FILING DATE: 1997-11-07
:   NUMBER OF SEQ ID NOS: 35
:   SOFTWARE: FastSeq for Windows Version 3.0
:   SEQ ID NO 20
:   LENGTH: 401
:   TYPE: PRN
:   ORGANISM: Saccharomyces cerevisiae
US-09-911-888-20

```

[illegible]

```

RESULT 9
US-09-911-927-20
: Sequence 20, Application US/09911927
: GENERAL INFORMATION:
: APPLICANT: Kollin, Yigal
: TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
: FILE REFERENCE: 06286-062003
: CURRENT APPLICATION NUMBER: US/09/911,927
: CURRENT FILING DATE: 2001-07-23
: PRIOR APPLICATION NUMBER: US 08/965,762
: PRIOR FILING DATE: 1997-11-07
: NUMBER OF SEQ ID NOS: 35
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 20
: LENGTH: 401
: TYPE: PRF
: ORGANISM: Saccharomyces cerevisiae
US-09-911-927-20

```

Query Match	34.38;	Score 75.5;	DB 6;	Length 401;
Best Local Similarity	39.58;	Pred. No. 0.011;		

Matches 15; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 6 ILTFVAAPFDDDDKLVHGKLNHHNNH---DDDDK 40
DB 38 VLADANSSIDAPFNKRKKRHHNNHHSRKEGNDK 75

RESULT 10
US-09-708-427-49415

; Sequence 49415, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49415
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc-feature
; LOCATION: 1..198
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc-feature
; LOCATION: 1..198
; OTHER INFORMATION: Ceres Seq. ID 1921855
US-09-708-427-49415

Query Match 33.6%; Score 74; DB 6; Length 198;
Best Local Similarity 36.2%; Pred. No. 0.0072;
Matches 17; Conservative 6; Mismatches 16; Indels 8; Gaps 1;

QY 1 NLLILTFVAAVAAPFDDDDKLVHGK-----LHHNNHDDDD 39
DB 6 VGVLLAAVAAALFAAARADDKQPMQCFRSCSGCHHHHHDDHNDN 52

RESULT 11
US-10-040-655-9
; Sequence 9, Application US/10040655
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/040,655
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: of Protease T in a zymogen activation construct
US-10-040-655-9

Query Match 33.6%; Score 74; DB 7; Length 315;
Best Local Similarity 52.8%; Pred. No. 0.013;
Matches 19; Conservative 2; Mismatches 5; Indels 10; Gaps 1;

QY 2 NLLILTFV-----AAVAAPFDDDDKLVHG 27
DB 20 NLLICGVSDYKDDDDVDAAALAAPFDDDDKIVG 55

RESULT 12
US-10-041-006-9

; Sequence 9, Application US/10041006
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/041,006
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: of Protease T in a zymogen activation construct
US-10-041-006-9

Query Match 33.6%; Score 74; DB 7; Length 315;
Best Local Similarity 52.8%; Pred. No. 0.013;
Matches 19; Conservative 2; Mismatches 5; Indels 10; Gaps 1;

QY 2 NLLILTFV-----AAVAAPFDDDDKLVHG 27
DB 20 NLLICGVSDYKDDDDVDAAALAAPFDDDDKIVG 55

RESULT 13
US-10-040-803-8
; Sequence 8, Application US/10040803
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew L.
; TITLE OF INVENTION: DNA encoding human serine protease C-E
; FILE REFERENCE: ORT-1030
; CURRENT APPLICATION NUMBER: US/10/040,803
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
; OTHER INFORMATION: domain fusion protein
US-10-040-803-8

Query Match 33.6%; Score 74; DB 7; Length 327;
Best Local Similarity 52.8%; Pred. No. 0.013;
Matches 19; Conservative 2; Mismatches 5; Indels 10; Gaps 1;

QY 2 NLLILTFV-----AAVAAPFDDDDKLVHG 27
DB 20 NLLICGVSDYKDDDDVDAAALAAPFDDDDKIVG 55

RESULT 14
US-09-620-111B-5168
; Sequence 5168, Application US/09620111B
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid

```

; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-1070P
; CURRENT APPLICATION NUMBER: US/09/620,11B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9298
; SEQ ID NO 5168
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..149
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..149
; OTHER INFORMATION: Ceres Seq. ID 1332728
US-09-620-11B-5168

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Query Match          32.7%; Score 72; DB 6; Length 149;
Best Local Similarity 42.1%; Pred. No. 0.0096;
Matches 16; Conservative 3; Mismatches 11; Indels 8; Gaps 1;

```

```

QY 10 VAAVAAPDDDKLVHGK-----LHHHHHDDDD 39
      ||| | ||| | : ||| | | :
DB 34 IAAATARAADDDDKTQPMQCFKSCSRGCHHHHDDHDN 71

```

```

RESULT 15
US-09-708-427-58802
; Sequence 58802, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58802
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..132
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..132
; OTHER INFORMATION: Ceres Seq. ID 1942723
US-09-708-427-58802

```

```

Query Match          32.3%; Score 71; DB 6; Length 132;
Best Local Similarity 78.6%; Pred. No. 0.011;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

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```

QY 26 HGKLIHHHHHDDDD 39
      || ||| ||| : |||
DB 94 HG--HHHHHDDDD 105

```

Search completed: March 15, 2002, 06:45:32
 Job time: 1146 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 06:26:26 ; Search time 12.51 seconds
(without alignments)
71.953 Million cell updates/sec

Title: US-09-856-050-19

Sequence: 1 MNLILITFYAAAVAFPDDDDKLVHGKLNHHHHDDDK 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
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3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	38.2	281	1 US-08-467-155A-7	Sequence 7, Appli
2	84	38.2	281	2 US-08-628-198-7	Sequence 7, Appli
3	84	38.2	281	4 US-09-201-038-7	Sequence 7, Appli
4	84	38.2	281	5 PCT-US96-07343-7	Sequence 7, Appli
5	81	36.8	246	2 US-08-978-404B-44	Sequence 44, Appli
6	75.5	34.3	401	4 US-08-965-762-20	Sequence 20, Appli
7	71	32.3	247	2 US-08-956-267A-2	Sequence 2, Appli
8	68	30.9	14	1 US-08-226-264-7	Sequence 7, Appli
9	68	30.9	14	1 US-08-226-264-19	Sequence 19, Appli
10	68	30.9	14	1 US-08-226-264-19	Sequence 19, Appli
11	68	30.9	16	1 US-08-226-264-8	Sequence 8, Appli
12	68	30.9	16	1 US-08-226-264-21	Sequence 21, Appli
13	67.5	30.7	280	4 US-09-214-095D-119	Sequence 119, App
14	66.5	30.2	24	3 US-08-584-031-8	Sequence 8, Appli
15	66.5	30.2	24	3 US-08-780-496-8	Sequence 8, Appli
16	66	30.0	20	1 US-08-416-336-4	Sequence 17, Appli
17	66	30.0	76	3 US-08-956-307B-17	Sequence 18, Appli
18	66	30.0	76	3 US-08-956-307B-18	Sequence 18, Appli
19	66	30.0	122	3 US-08-956-307B-19	Sequence 19, Appli
20	65.5	29.8	17	3 US-09-136-421-10	Sequence 10, Appli
21	65.5	29.8	18	1 US-08-578-649-14	Sequence 14, Appli
22	65.5	29.8	18	1 US-08-670-175-8	Sequence 8, Appli
23	65.5	29.8	29	5 PCT-US94-05150-37	Sequence 37, Appli
24	64.5	29.3	254	3 US-09-167-434-7	Sequence 7, Appli
25	64.5	29.3	254	3 US-08-853-755-7	Sequence 4, Appli
26	64	29.1	211	4 US-08-856-253-4	Sequence 19, Appli
27	62.5	28.4	53	2 US-08-651-818A-19	

28	62.5	28.4	53	4 US-09-184-826-19	Sequence 19, Appli
29	62.5	28.4	54	2 US-08-651-818A-23	Sequence 23, Appli
30	62.5	28.4	54	4 US-09-184-826-23	Sequence 23, Appli
31	62.5	28.4	335	4 US-09-095-117-2	Sequence 2, Appli
32	62.5	28.4	335	4 US-09-095-117-4	Sequence 4, Appli
33	62	28.2	43	2 US-08-652-816A-43	Sequence 43, Appli
34	62	28.2	68	1 US-08-530-638D-2	Sequence 2, Appli
35	62	28.2	68	2 US-08-906-746A-2	Sequence 2, Appli
36	62	28.2	397	3 US-08-978-741-6	Sequence 6, Appli
37	62	28.2	397	4 US-09-333-729A-7	Sequence 7, Appli
38	62	28.2	492	2 US-08-644-271-32	Sequence 32, Appli
39	61	27.7	10	4 US-09-197-801-14	Sequence 14, Appli
40	61	27.7	10	4 US-09-551-028-14	Sequence 14, Appli
41	61	27.7	10	4 US-09-202-101-17	Sequence 17, Appli
42	61	27.7	301	2 US-08-661-052-14	Sequence 14, Appli
43	61	27.7	301	4 US-09-188-082-14	Sequence 14, Appli
44	61	27.7	391	5 PCT-US95-15696-2	Sequence 2, Appli
45	61	27.7	448	4 US-09-461-474-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-467-155A-7
; Sequence 7, Application US/08467155A
; Patent No. 5736377
; GENERAL INFORMATION:
; APPLICANT: Band, Viola
; TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
; NUMBER OF INVENTIONS: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,155A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00398/100001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-8906
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-155A-7

Query Match 38.2%; Score 84; DB 1; Length 281;
Best local similarity 66.7%; Pred. No. 0.00025;
Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MNLILITFYAAAVAFPDDDDKLVHG 27
DB 1 MSALLITLVAAGAAVAFPDDDDKIVG 27

Query Match 32.3%; Score 71; DB 2; Length 247;
Best Local Similarity 53.8%; Pred. No. 0.014;
Matches 14; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 NLLILFVAAVAAPFDDDKLVHG 27
Db 3 NTFVLLALGAAVAFPTDDDKIVGG 28

RESULT 8

US-08-226-264-7
; Sequence 7, Application US/08226264
; Patent No. 5801017
; GENERAL INFORMATION:
; APPLICANT: Werber, Moshe M.
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Levanon, Avigdor
; APPLICANT: Guy, Rachel
; APPLICANT: Goldlust, Arle
; APPLICANT: Rigbi, Meir
; APPLICANT: Panet, Amos
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
; TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/226,264
; FILING DATE: 08-APR-94
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-226-264-7

Query Match 30.9%; Score 68; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.0012;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 29 LHHHHH--DDDDK 40
Db 1 MHHHHHGTDDDK 14

RESULT 9

US-08-226-264-19
; Sequence 19, Application US/08226264
; Patent No. 5801017
; GENERAL INFORMATION:
; APPLICANT: Werber, Moshe M.
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Levanon, Avigdor
; APPLICANT: Guy, Rachel
; APPLICANT: Goldlust, Arle
; APPLICANT: Rigbi, Meir
; APPLICANT: Panet, Amos
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
; TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/226,264
; FILING DATE: 08-APR-94
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-226-264-19

Query Match 30.9%; Score 68; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.0012;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 29 LHHHHH--DDDDK 40
Db 1 MHHHHHGTDDDK 14

RESULT 10

US-08-226-264-20
; Sequence 20, Application US/08226264
; Patent No. 5801017
; GENERAL INFORMATION:
; APPLICANT: Werber, Moshe M.
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Levanon, Avigdor
; APPLICANT: Guy, Rachel
; APPLICANT: Goldlust, Arle
; APPLICANT: Rigbi, Meir
; APPLICANT: Panet, Amos

APPLICANT: Fischer, Meir
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/226,264
FILING DATE: 08-APR-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-226-264-20

Query Match 30.9%; Score 68; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.0012;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 29 LHHHHH--DDDK 40
DB 1 MHHHHHGTDDDK 14

RESULT 11
US-08-226-264-8
Sequence 8, Application US/08226264
Patent No. 5801017
GENERAL INFORMATION:
APPLICANT: Werber, Moshe M.
APPLICANT: Zeelon, Elisha P.
APPLICANT: Levanon, Avigdor
APPLICANT: Guy, Rachel
APPLICANT: Goldlust, Arle
APPLICANT: Rigbi, Meir
APPLICANT: Panet, Amos
APPLICANT: Fischer, Meir
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/226,264
FILING DATE: 08-APR-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-226-264-8

Query Match 30.9%; Score 68; DB 1; Length 16;
Best Local Similarity 78.6%; Pred. No. 0.0014;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 29 LHHHHH--DDDK 40
DB 1 MHHHHHGTDDDK 14

RESULT 12
US-08-226-264-21
Sequence 21, Application US/08226264
Patent No. 5801017
GENERAL INFORMATION:
APPLICANT: Werber, Moshe M.
APPLICANT: Zeelon, Elisha P.
APPLICANT: Levanon, Avigdor
APPLICANT: Guy, Rachel
APPLICANT: Goldlust, Arle
APPLICANT: Rigbi, Meir
APPLICANT: Panet, Amos
APPLICANT: Fischer, Meir
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/226,264
FILING DATE: 08-APR-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.

REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 TELEX:
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-08-226-264-21

Query Match 30.9%; Score 68; DB 1; Length 16;
 Best Local Similarity 78.6%; Pred. No. 0.0014;
 Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 29 LHHHHH-DDDDK 40
 :|||||
 DB 1 MHHHHGTDGDDK 14

RESULT 13
 US-09-214-095D-119
 ; Sequence 119, Application US/09214095D
 ; Patent No. 6280987
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 51400-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/214, 095D
 ; CURRENT FILING DATE: 1999-07-19
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 119
 ; LENGTH: 280
 ; TYPE: PRT
 ; ORGANISM: Murine
 ; US-09-214-095D-119

Query Match 30.7%; Score 67.5; DB 4; Length 280;
 Best Local Similarity 75.0%; Pred. No. 0.05;
 Matches 12; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 19 DDDDKLVHGLHHH 34
 :|||||
 DB 268 DDDDKLVHGLHHH 280

RESULT 14
 US-08-584-031-8
 ; Sequence 8, Application US/08584031A
 ; Patent No. 6030945
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: APO-2 LIGAND
 ; FILE REFERENCE: 11669, 22US03
 ; CURRENT APPLICATION NUMBER: US/08/584, 031A
 ; CURRENT FILING DATE: 1996-01-09
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 24
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

NAME/KEY: UNSURE
 LOCATION: (1)..(24)
 OTHER INFORMATION: Sequence is synthesized
 ; Patent No. 6030945
 ; US-08-584-031-8

Query Match 30.2%; Score 66.5; DB 3; Length 24;
 Best Local Similarity 60.0%; Pred. No. 0.0036;
 Matches 12; Conservative 0; Mismatches 3; Indels 5; Gaps 1;

QY 26 HGKLVHHH-----DDDDK 40
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 DB 3 HHHHHHHHSSGHIDDDK 22

RESULT 15
 US-08-780-496-8
 ; Sequence 8, Application US/08780496
 ; Patent No. 6046048
 ; GENERAL INFORMATION:
 ; APPLICANT: Avi Ashkenazi, Anan Chuntcharapai, Kyung Jin Kim
 ; TITLE OF INVENTION: APO-2 Ligand
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Winpatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/780,496
 ; FILING DATE: 08-Jan-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Marschang, Diane L.
 ; REGISTRATION NUMBER: 35,600
 ; REFERENCE/DOCKET NUMBER: P0978P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-5416
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 24 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: linear
 ; US-08-780-496-8

Query Match 30.2%; Score 66.5; DB 3; Length 24;
 Best Local Similarity 60.0%; Pred. No. 0.0036;
 Matches 12; Conservative 0; Mismatches 3; Indels 5; Gaps 1;

QY 26 HGKLVHHH-----DDDDK 40
 :|||||
 DB 3 HHHHHHHHSSGHIDDDK 22

Search completed: March 15, 2002, 06:44:18
 Job time: 1072 sec

Fri Mar 15 06:40:14 2002

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